

A<sup>1</sup>  
3. The method of claim 20, wherein said DNA is non-genomic DNA.

4. The method of claim 20, wherein said DNA is cDNA.

Sub B1  
A<sup>2</sup>  
20. A method of subjecting a DNA molecule to a DNA synthesis reaction, the DNA molecule having a first linker sequence positioned at one end of the DNA molecule and a second linker sequence, different from said first linker sequence, positioned at the other end of the DNA molecule, wherein said DNA is subjected to a DNA synthesis reaction with a primer set comprising:

- a) a first primer, wherein the 5' sequence of said primer is complementary to said first linker sequence and the 3' sequence of said primer comprises a specificity region;
- b) a second primer, wherein the 5' sequence of said primer is complementary to said second linker sequence and the 3' sequence of said primer comprises a specificity region.

84  
21. The method of claim 85, wherein said amplification is performed with an array of combinations of alternate amplification primers.

A<sup>3</sup>  
23. The method of claim 85, further comprising, identifying the amplified DNA.

A<sup>4</sup>  
29. The method of claim 85, wherein said amplification comprises polymerase chain reaction, nucleic acid sequence based amplification, transcription mediated amplification, strand displacement amplification or ligase chain reaction.

A<sup>5</sup>  
36. The method of claim 85, wherein a label is incorporated into said amplified DNA.

A<sup>6</sup>  
45. The method of claim 20, wherein the products of said DNA synthesis reaction are analyzed.

46. The method of claim 45, wherein said analysis of products is by polyacrylamide gel electrophoresis.
47. The method of claim 45, wherein said analysis of products is by capillary gel electrophoresis.
48. The method of claim 45, wherein said analysis of products is by mass spectrophotometry.
49. The method of claim 45, wherein said analysis of products is by energy transfer.
50. The method of claim 45, wherein said analysis of products is by the BioStar technology.
51. The method of claim 45, wherein said analysis of products is by the Luminex technology.
52. The method of claim 45, wherein said analysis of products comprises quantifying amplification products.
53. The method of claim 52, wherein said quantifying is by measuring the ratio of each product to a co-amplified reference-gene.
54. The method of claim 52, wherein said quantifying is by measuring the ratio of each product to a panel of reference-genes.
55. The method of claim 52, wherein said analysis of products is by Real-Time PCR.
56. The method of claim 45, wherein said analysis of products is performed in a multi-well plate.
57. The method of claim 45, wherein said analysis of products is performed on a membrane.

58. The method of claim 45, wherein said analysis of products is performed on a solid matrice.

59. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a different cell or tissue.

60. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cancerous cell or tissue.

61. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a pharmaceutical compound.

62. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a teratogenic compound.

63. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a carcinogenic compound.

64. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a toxic compound.

65. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a biological response modifier.

66. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a hormone, a hormone agonist or a hormone antagonist.

67. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a cytokine.

69. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a growth factor.

70. The method of claim 20, performed on DNA derived from a normal cell or tissue and on the DNA derived from a cell or tissue treated with the ligand of a known biological receptor.

Sub B3  
71. The method of claim 20, performed on DNA derived from a cell or tissue type obtained from a different species.

Cont  
A6  
72. The method of claim 20, performed on DNA derived from a cell or tissue type obtained from a different organism.

73. The method of claim 20, performed on DNA derived from a cell or tissue at different stages of development.

74. The method of claim 20, performed on DNA derived from a normal cell or tissue and on the DNA derived from a cell or tissue that is diseased.

75. The method of claim 20, performed on DNA derived from a cell or tissue cultured in vitro under different conditions.

76. The method of claim 20, performed on the DNA derived from a cell or tissue from two organisms of the same species with a known genetic difference.

---

Please add the following new claims, claim 85 and 89:

---

A7  
85. The method of claim 20, wherein the first and second primers are employed to amplify the DNA molecule.

86. The method of claim 20, wherein the first and second primers are employed to sequence the DNA molecule.

Cont  
A<sup>7</sup> SubB4  
87. A primer molecule having a 5' sequence for annealing to a linker sequence and a 3' terminal specificity region of from 3 to 8 nucleotides in length, the specificity region defined as one of all possible sequence combinations of A, T, G and C.

88. A population of primer molecules, the primer molecules having a 5' sequence for annealing to a linker sequence and a 3' terminal specificity region of from 3 to 8 nucleotides in length, the population of primer molecules having specificity regions collectively reflecting all possible sequence combinations of A, T, G and C.

89. A primer molecule selected from the population of claim 88.

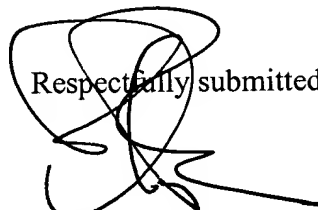
---

#### REMARKS

The Examiner is requested to enter the above claim amendments before examination of the case. The claims now focus on the aspect of initial claim 20, previously a dependant claim and now made the principal independent claim. The method of claim 20 is no longer tied to the method of claim 1, and focuses in on Applicant's novel use of primer having a "specificity region" (*i.e.*, a primer that will anneal to a linker region and also has a region that will define specific hybridization to a region on the DNA molecule).

Support for new claims 87-89 can be found in the specification at the top of page 21.

If the Examiner has any questions or comments, a telephone call to the undersigned at  
(512) 536-3055 is requested.

Respectfully submitted,  


David L. Parker  
Reg. No. 32,165  
Attorney for Applicant

FULBRIGHT & JAWORSKI L.L.P.  
600 Congress Avenue, Suite 2400  
Austin, Texas 78701  
512/536-3055

Date: September 26, 2001